VSFRLSGATTTSY, FRLSGATTTSYGV, TSYGVFIKNLREA, YGVFIKNLREALP, GVFIKNLREALPY, VFIKNLREALPYE, KNLREALPYERKV, EALPYERKVYNIP, LPYERKVYNIPLL, RKVYNIPLLRSSI, KVYNIPLLRSSIS, YNIPLLRSSISGS, IPLLRSSISGSGR, PLLRSSISGSGRY, SSISGSGRYTLLH, GRYTLLHLTNYAD, YTLLHLTNYADET, TLLHLTNYADETI, LHLTNYADETISV, TNYADETISVAVD, ETISVAVDVTNVY, VAVDVTNVYIMGY, ISVAVDVTNVYIM, VDVTNVYIMGYLA, TNVYIMGYLAGDV, NVYIMGYLAGDVS, VYIMGYLAGDVSY, YIMGYLAGDVSYF, MGYLAGDVSYFFN, GYLAGDVSYFFNE, GDVSYFFNEASAT, VSYFFNEASATEA, SYFFNEASATEAA, YFFNEASATEAAK, AKFVFKDAKKKVT, KFVFKDAKKKVTL, FVFKDAKKKVTLP, KKVTLPYSGNYER, VTLPYSGNYERLQ, LPYSGNYERLQTA, GNYERLQTAAGKI, ERLQTAAGKIREN, GKIRENIPLGLPA, ENIPLGLPALDSA, IPLGLPALDSAIT, LGLPALDSAITTL, PALDSAITTLYYY, SAITTLYYYTASS, TTLYYYTASSAAS, TLYYYTASSAASA, LYYYTASSAASAL, · St. YYYTASSAASALL, SALLVLIQSTAES, ALLVLIQSTAESA, LVLIQSTAESARY, LLVLIQSTAESAR, VLIQSTAESARYK, ARYKFIEQQIGKR, YKFIEQQIGKRVD, KFIEQQIGKRVDK, QQIGKRVDKTFLP, KRVDKTFLPSLAT, KTFLPSLATISLE, TFLPSLATISLEN, PSLATISLENNWS, ATISLENNWSALS, ISLENNWSALSKQ, NNWSALSKQIQIA, SALSKQIQIASTN, KQIQIASTNNGQF, IQIASTNNGQFES, GQFESPVVLIDGN, SPVVLIDGNNQRV, PVVLIDGNNQRVS, VVLIDGNNQRVSI, VLIDGNNQRVSIT, QRVSITNASARVV, VSITNASARVVTS, ARVVTSNIALLLN, RVVTSNIALLLNR, SNIALLLNRNNIA, IALLLNRNNIAAI, ALLLNRNNIAAIG, LLLNRNNIAAIGE, NNIAAIGEDISMT, AAIGEDISMTLIG, EDISMTLIGFEHG, TSMTLIGFEHGLY, MTLIGFEHGLYGI,

Peptide ID #	Bryodin1; 15mer peptide sequence	Residue #
1	DVSFRLSGATTTSYG	1
2	FRLSGATTTSYGVFI	4
3	SGATTTSYGVFIKNL	7
4	TTTSYGVFIKNLREA	10
5	Sygvfiknlrealpy	13
6	VFIKNLREALPYERK	16
7	KNLREALPYERKVYN	19
8	REALPYERKVYNIPL	22
9	LPYERKVYNIPLLRS	25
10	ERKVYNIPLLRSSIS	28
11	VYNIPLLRSSISGSG	31
12	IPLLRSSISGSGRYT	34
13	LRSSISGSGRYTLLH	37
14	SISGSGRYTLLHLTN	40
15	GSGRYTLLHLTNYAD	43
16	RYTLLHLTNYADETI	46
17	LLHLTNYADETISVA	49
18	LTNYADETISVAVDV	52
19	YADETISVAVDVTNV	55
20	ETISVAVDVTNVYIM	58
21	SVAVDVTNVYIMGYL	61
22	VDVTNVYIMGYLAGD	64
23	TNVYIMGYLAGDVSY	67
24	YIMGYLAGDVSYFFN	70
25	GYLAGDVSYFFNEAS	73
26	AGDVSYFFNEASATE	76
27	VSYFFNEASATEAAK	79
28	FFNEASATEAAKFVF	82
29	EASATEAAKFVFKDA	85
30	ATEAAKFVFKDAKKK	88
31	AAKFVFKDAKKKVTL	91
32	FVFKDAKKKVTLPYS	94
33	KDAKKKVTLPYSGNY	97
34	KKKVTLPYSGNYERL	100
35	VTLPYSGNYERLOTA	103
36	PYSGNYERLQTAAGK	106
37	GNYERLQTAAGKIRE	109
38	ERLQTAAGKIRENIP	112
39	QTAAGKIRENIPLGL	115
40	AGKIRENIPLGLPAL	118
41	IRENIPLGLPALDSA	121
42	NIPLGLPALDSAITT	124
43	LGLPALDSAITTLYY	127

Peptide ID#	Bryodin1; 15mer peptide sequence	Residue #
44	PALDSAITTLYYYTA	130
45	DSAITTLYYYTASSA	133
46	ITTLYYYTASSAASA	136
47	LYYYTASSAASALLV	139
48	YTASSAASALLVLIQ	142
49	SSAASALLVLIQSTA	145
50	ASALLVLIQSTAESA	148
51	LLVLIQSTAESARYK	151
52	LIQSTAESARYKFIE	154
53	STAESARYKFIEQQI	157
54	ESARYKFIEQQIGKR	160
55	RYKFIEQQIGKRVDK	163
56	FIEQQIGKRVDKTFL	166
57	QQIGKRVDKTFLPSL	169
58	GKRVDKTFLPSLATI	172
59	VDKTFLPSLATISLE	175
60	TFLPSLATISLENNW	178
61	PSLATISLENNWSAL	181
62	ATISLENNWSALSKQ	184
63	SLENNWSALSKQIQI	187
64	NNWSALSKQIQIAST	190
65	SALSKQIQIASTNNG	193
66	SKQIQIASTNNGQFE	196
67	IQIASTNNGQFESPV	199
68	ASTNNGQFESPVVLI	202
69	NNGQFESPVVLIDGN	205
70	QFESPVVLIDGNNQR	208
71	SPVVLIDGNNQRVSI	211
72	VLIDGNNQRVSITNA	. 214
73	DGNNQRVSITNASAR	217
74	NQRVSITNASARVVT	220
·75	VSITNASARVVTSNI	223
76	TNASARVVTSNIALL	226
77	SARVVTSNIALLLNR	229
78	VVTSNIALLLNRNNI	232
79	SNIALLLNRNNIAAI	235
80	ALLLNRNNIAAIGED	238
81	LNRNNIAAIGEDISM	241
82	NNIAAIGEDISMTLI	244
83	AAIGEDISMTLIGFE	247
84	GEDISMTLIGFEHGL	250
85	ISMTLIGFEHGLYGI	253

Epitope R1 (residues 46-66)

1BRY	RYTLLHLTNYADETISVAVDV
1TCS	::A:I:::::::::::::::::::::::::::::::::
1CF5	:FI:::::S::Y:::::::

Epitope R2 (residues 88-102)

1BRY	ATEAAKFVFKDAKK										
1TCS	:::::Y:::::MR:										

Epitope R3 (residues 112-135)

1BRY	ERLQTAAGKIRENIPLGLPALDSA
1TCS	
1CF5	:N:::::H::::::::::::::::::::::::::::::
1MOM	·::::I::::P::K::I::::::

Epitope R4 (residues 136-162)

1BRY	ITTLYYYTASSAASALLVLIQSTAESA
1TCS	::::F:::N:N::::::M::::::S:A:
1CF5	::::F::N:Q::P::::::T:::A:
1MOM	:S::LH:DSTA::G:::::T:::A:

Epitope R5 (residues 178-204)

1BRY	ATISLENNWSALSKQIQIAST
1TCS	:I::::S:::::::::::::
1CF5	:I::::Q::::::::FL:QN
1MOM	::::::::S:::G::::::L:QG

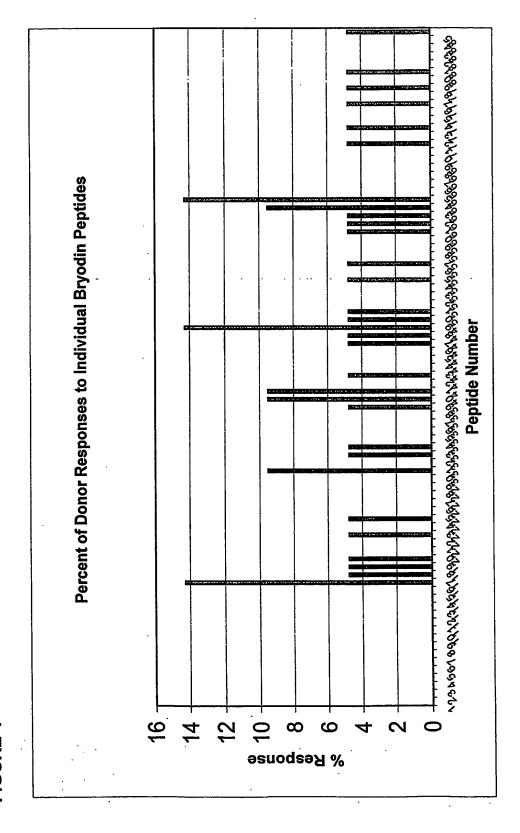
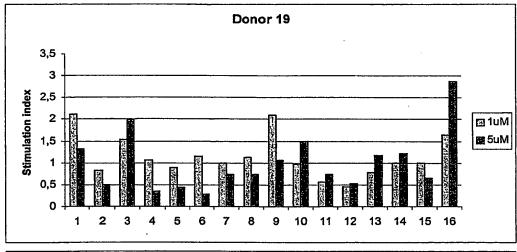
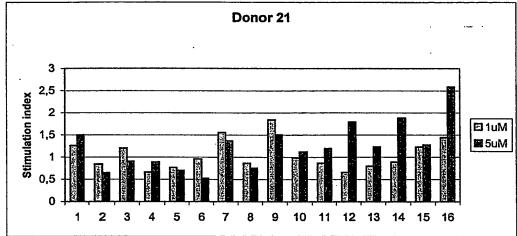
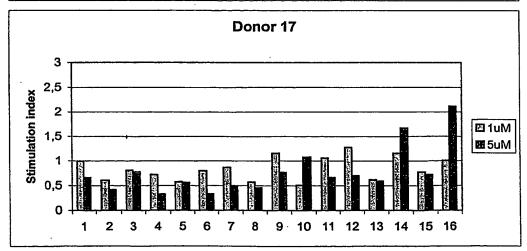


FIGURE 4

FIGURE 5 A



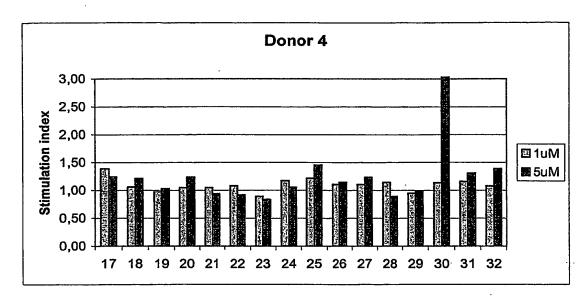


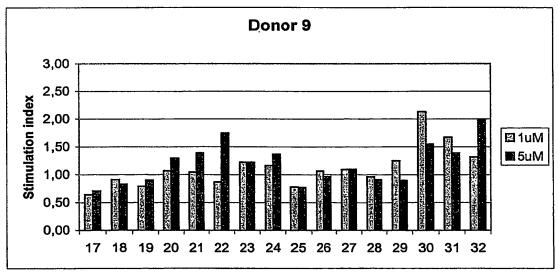


PBMC donor response charts to bryodin 1 peptides #1 –16 Peptide #16 is encompassed within epitope region R1

PCT/EP03/06055

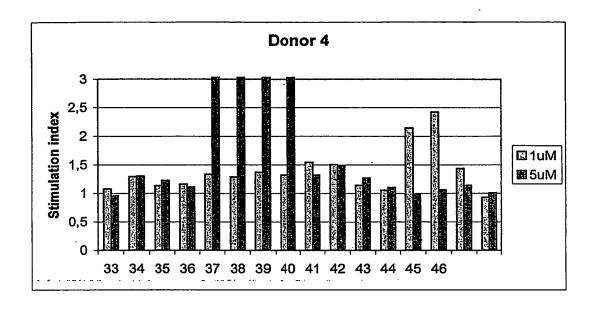
FIGURE 5 B

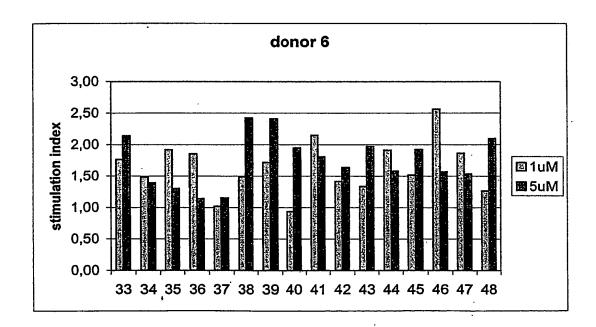




PBMC donor response charts to bryodin 1 peptides #17 - 32 Peptide #30 is encompassed within epitope region R2

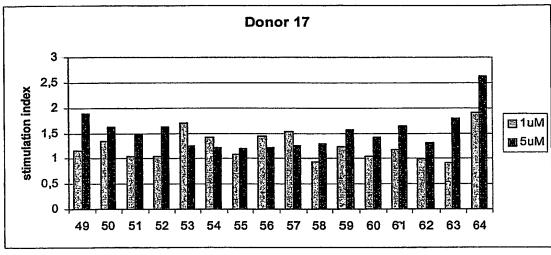
FIGURE 5 C

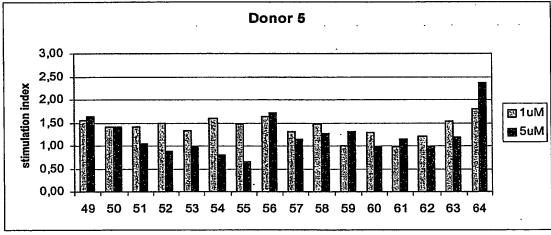


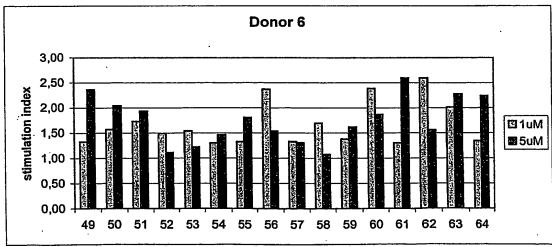


PBMC donor response charts to bryodin 1 peptides #33-48 Peptides #39 and #40 are encom[passed within epitope region R3.

FIGURE 5 D







PBMC donor response charts to bryodin 1 peptides #49 - 64 Peptide #64 is encompassed within epitope region R5

MHC Class II ligands detected within epitope region R1

							20.01		=0.0=		== 00	40	=0.00	¥0.42				
13.21 13.21	25.32 12.11	37.10 11.77	44.75 7.65	52.22 7.48	58.03 5.81	63.21 5.17	66.94 3.73	69.65 2.71	72.07 2.42	74.41 2.34	75.80 1.39	77.10 1.3	78.09 0.99	79.06 0.97				
701	3011	15011	401	101	1301	11011	302	1401	103	801	1602	1201	9011	1001	3*0202	4*01011	- 5*0101	
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			emach Special Specia Specia Specia Specia Specia Specia Specia Specia Specia S	1,1,20 1,20			Constant Cons						****	And the second s		****		
	(2) (2) (2) (2) (2) (2) (2) (2) (2) (2)			10 to			A Company of the Comp	A PER A PER				Comment Commen	0000460 000000		() () () () () () () () () ()	A Section 1		

	701	701	13.21 12.11 11.77 701 3011 3011	13.21 12.11 11.77 7.65 701 3011	13.21 12.11 11.77 7.65 7.48 701 15011 1 1.77 7.65 7.48	13.21 12.11 11.77 7.65 7.48 5.81 701 15011 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	13.21 12.11 11.77 7.65 7.48 5.81 5.17 701 15011 1.77 7.65 7.48 5.81 5.17	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 701 15011	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 701 15011	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 70.1 15011 70.1 1.5011 70.1	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 70.1 1.501.1	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 14.01 1.01 1.01 1.01 1.01 1.01 1.01 1.01	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 701 15011 101	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 701 15011 10	1321 1211 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 1001 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1321 1211 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 701 15011 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97	1321 1211 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 1001	1321 1211 11.77 7.65 7.88 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 5*01011 13011 13011 13011

LEGEND

>1000K

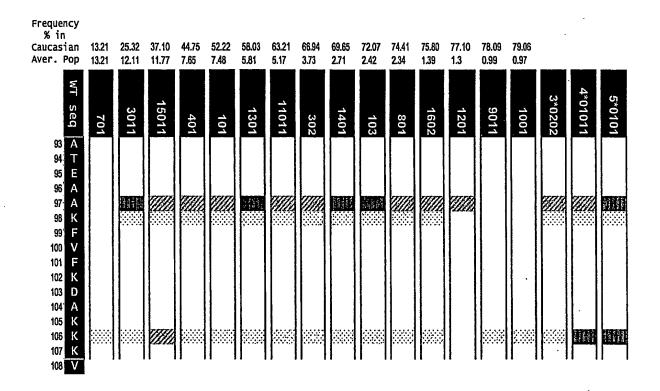
750K-1000K

500K-750K

PCT/EP03/06055

FIGURE 7

MHC Class II ligands detected within epitope region R2



LEGEND

>1000K

750K-1000K

500K-750K

MHC Class II ligands detected within epitope region R3

Frequency %												•						
Caucasian Aver. Pop	13.21 13.21	25.32 12.11	37.10 11.77	44.75 7.65	52.22 7.48	58.03 5.81	63.21 5.17	66.94 3.73	69.65 2.71	65.63 2.42	71.99 2.34	73.38 1.39	74.68 1.3	75.67 0.99	76.64 0.97			
WT Seq 113 E 114 R 115 L 116 Q 117 T	701	3011	15011	401	101	1301	11011	302	1401	103	801	1602	1201	9011	1001	3*0202	4*01011	5*0101
118 A 119 A 120 G 121 K 122 I				双排作	TE a.	esi			To the state of th	-135			100				114	
123 R 124 E 125 N 126 I 127 P							288											
128 L 129 G 130 L																		
131 P 132 A 133 L																		
134 D 135 S 136 A		相称	E ST	PER.							ili.		1844					

LEGEND

>1000K 750K-1000K 500K-750K

MHC Class II ligands detected within epitope region R4

13.21 13.21	25.32 12.11	37.10 11.77	44.75 7.65	52.22 7.48	58.03 5.81	63.21 5.17	66.94 3.73	69.65 2.71	65.63 2.42	71.99 2.34	73.38 1.39	74.68 1.3	75.67 0.99	76.64 0.97			
701	3011	15011	401	101	1301	11011	302	1401	103	801	1602	1201	9011	1001	3*0202	4*01011	5*0101
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	13.21	701	13.21 12.11 11.77 15.01.11 3.01 3.0	701 12.11 11.77 7.65 401	701 12.11 11.77 7.65 7.48 101 101 11.77 7.65 7.48	701 12.11 11.77 7.55 7.48 5.81 13.01 1 1.77 7.55 7.48 5.81	701 12.11 11.77 7.65 7.48 5.81 5.17 11011 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 701 15011 101 <td>1321 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 1301 11 11.77 7.65 7.48 5.81 5.17 3.73 2.71</td> <td>13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1</td> <td>1321 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1301 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1</td> <td>13.21 12.11 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 701 3011 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39</td> <td>13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3</td> <td>13.21 12.11 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 9011 701 1501 101 101 101 101 101</td> <td>13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 701 13.01 13</td> <td>13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 100.1</td> <td>13.21 12.11 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 10001 17.1</td>	1321 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 1301 11 11.77 7.65 7.48 5.81 5.17 3.73 2.71	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1321 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1301 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	13.21 12.11 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 701 3011 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3	13.21 12.11 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 9011 701 1501 101 101 101 101 101	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 701 13.01 13	13.21 12.11 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 7.65 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 100.1 11.77 100.1	13.21 12.11 11.77 7.55 7.48 5.81 5.17 3.73 2.71 2.42 2.34 1.39 1.3 0.99 0.97 10001 17.1

LEGEND



MHC Class II ligands detected within epitope region R5

Frequency %																		
Caucasian Aver. Pop	13.21 13.21	25.32 12.11	37.10 11.77	44.7 <u>.</u> 5 7.65	52.22 7.48	58.03 5.81	63.21 5.17	66.94 3.73	69.65 2.71	65.63 2.42	71.99 2.34	73.38 1.39	74.68 1.3	75.67 0.99	76.64 0.97			
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>1000K 750K-1000K 500K-750K